

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.
OM protein - protein search, using sw model
Run on: March 14, 2001, 16:12:19 ; Search time 21.02 Seconds
(without alignments)
1466.551 Million cell updates/sec
Title: US-09-455-486-6
Perfect score: 2351
Sequence: 1 MESISMGSPKSLSETCLPN.....ALVLPISVILDLQLCRYPD 454
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 195891 seqs, 67900655 residues
Total number of hits satisfying chosen parameters: 195891
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : PIR_66.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	156.5	6.7	239	2 T50571	probable oxidoreductase
2	147	6.3	213	2 H69400	conserved hypothetical
3	142	6.0	212	2 D69361	conserved hypothetical
4	142	6.0	224	2 T10120	F420-dependent NAD
5	133	5.7	223	2 D64487	hypothetical prote
6	120.5	5.1	232	2 A69131	conserved hypothetical
7	119.5	5.1	216	2 T00121	hypothetical prote
8	116.5	5.0	242	2 G82642	conserved hypothetical
9	111.5	4.7	695	1 JN0898	foliitropin recept
10	111.5	4.7	1228	2 S59681	probable membrane
11	110.5	4.7	694	2 JC4301	foliitropin recept
12	109	4.6	320	2 T28379	ORF MSV218 hypothe
13	109	4.6	712	2 S50969	probable membrane
14	109	4.6	1184	2 H71436	hypothetical prote
15	107.5	4.6	629	2 S60385	probable membrane
16	107.5	4.6	695	1 QRHUT	foliitropin recept
17	105	4.5	442	2 B64582	sodium- and chlori
18	105	4.5	604	2 T31042	hypothetical prote
19	104	4.4	396	1 C64907	chloramphenicol re
20	103	4.4	465	2 S69915	sodium-phosphate t
21	102.5	4.4	1242	2 T39453	probable mrna stab
22	102	4.3	574	2 T41068	hypothetical prote
23	101	4.3	320	2 E71139	hypothetical prote
24	101	4.3	348	2 T12284	NADH dehydrogenase
25	101	4.3	420	2 F69144	O-antigen transpor
26	101	4.3	501	2 T02134	hypothetical prote
27	101	4.3	735	2 A83006	hypothetical prote
28	100.5	4.3	346	2 T11181	NADH dehydrogenase
29	100	4.3	395	2 C71219	hypothetical prote

30 100 4.3 476 2 A28439 endonuclease SceI
31 99.5 4.2 452 2 C71391 NADH dehydrogenase
32 98 4.2 348 2 T12290 NADH dehydrogenase
33 98 4.2 348 2 T12281 NADH dehydrogenase
34 98 4.2 442 2 G71930 probable transport
35 98 4.2 962 2 T05845 hypothetical prote
36 98 4.2 3411 1 GNWVY genome polyprotein
37 98 4.2 3411 1 GNWVY genome polyprotein
38 97.5 4.1 268 2 A70417 hypothetical prote
39 97.5 4.1 695 2 I45896 follicle stimulat
40 97 4.1 346 2 T11325 NADH dehydrogenase
41 97 4.1 348 2 T12283 NADH dehydrogenase
42 97 4.1 692 2 A34548 foliitropin recept
43 96.5 4.1 608 2 G02640 polycystic kidney
44 96.5 4.1 686 2 S30075 ferric reductase
45 96.5 4.1 711 2 T25281 hypothetical prote

ALIGNMENTS

RESULT 1
T50571
Probable oxidoreductase [imported] - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 28-Jul-2000
C:Accession: T50571
R:Redenbach, M.; Kieser, H.M.; Denapalite, D.; Eichner, A.; Cullum, J.; Kinashi, H.; H
Mol. Microbiol. 21, 77-96, 1996
A:Title: A set of ordered cosmids and a detailed genetic and physical map for the 8 M.
A:Reference number: Z20556; MUID:97000351
A:Accession: T50571
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-239 <RED>
A:Cross-references: EMBL:AL133220; PIDN:CAB61708.1
A:Experimental source: strain A3(2)
C:Genetics:
A:Note: SCC75A.08c
C:Superfamily: conserved hypothetical protein MJ1501

Query Match 6.7%; Score 156.5; DB 2; Length 239;
Best Local Similarity 27.9%; Pred. No. 3.5e-05;
Matches 61; Conservative 41; Mismatches 72; Indels 45; Gaps 10;
Qy 25 IKDARKVTGVVI-GSGDFAKSLTIRLCGYHVVGSR---NPKFASEFFHHVVDVTHHE 80
Db 23 LPDVSGLVVGVLGGTGGPOGKGLAYRLAKAGKVIIVGSRAAERAAAAEEIGHGVEGADNA 82
Qy 81 DALTKTNIIFVAIHR-HYTSLWDLRLHLLVGLKILIDVSNMNRINO-----YPE--SNAE 131
Db 83 ETARSDVIVAVPMDHGKGTLESRLAELSGKLVYDVCNPLGFKKGYALKPEGSAAE 142
Qy 132 YLASLPDPSLVKGVNVVSANALQ-----LGPKDASQVYICSNIIQARQOV 178
Db 143 QAAALLPDSRAAAPHLSVALLQDPDEIDTDMVLGEERADVEI-----VQA----- 192
Qy 179 IELARQLNFIP-----IDGLSLSSAREIENLPLRFLTLWR 213
Db 193 --LAGR---IPGMRGVFAFGLRNNAHQVESLVANLISVNR 226

RESULT 2
H69400
conserved hypothetical protein AF1209 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
C:Accession: H69400
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997

Db 188 VESLTPILNIMR 200

RESULT 4
T10120
F420-dependent NADP reductase (EC 1.6.8.-) - Methanobacterium thermoautotrophicum (str. F420)
C:Species: Methanobacterium thermoautotrophicum
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
C:Accession: T10120
R:Berk, H.; Thauer, R.K.
FEBS Lett. 438, 124-126, 1998
A:Title: F420H2:NADP oxidoreductase from Methanobacterium thermoautotrophicum: identical
A:Reference number: Z16959; MUID:99037734
A:Accession: T10120
A:Status: preliminary; translated from GB/EMBL/DBJ /
A:Molecule type: DNA
A:Residues: 1-224 <BER>
A:Cross-references: EMBL:Y17210
A:Experimental source: strain Marburg
C:Superfamily: conserved hypothetical protein MJ1501
C:keywords: oxidoreductase

Query Match 6.0%; Score 142; DB 2; Length 224;
Best Local Similarity 29.2%; Pred. NO. 0.00046;
Matches 59; Conservative 29; Mismatches 84; Indels 30; Gaps 8;

Qy 37 GSGDFAKSLIRLCIRCGYHVVGISRNPKFASEFPFHVVDVTHHEDALTK--TN----- 87
Db 8 GTGDQGGGLALRCALAGEEVIIGSRDAEKAVSAAQKVLKLEIAERDLDLVKVGATNAEAAEEA 67
Qy 88 ---IIFVAIHREHYTSLWDLRHLVLGVKILIDV-----SNNMRINQVPSNAEYLA 134
Db 68 EVALLTPLOAQMAT-LGSVKEAIKGVKLVLDATVPIDSCLGGSNAVRYIDLWDSAAERAA 126
Qy 135 SLFPD--SLIVKGFNVYSAWALO--LGPKDASROVYICSNIIQARQOVIELARQLNFI-P 189
Db 127 RFLDQGTTRVAAAFNNISASALLDITGPVDC--DCLIASDRDALLDLASELAEKIDGVRA 184
Qy 190 IDLGSLSASAREINPLRLFTL 211
Db 185 IDCGGLENAKVIEKITPLNLN 206

RESULT 5
D64487
hypothetical protein MJ1501 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: D64487
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Black
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999
A:Accession: D64487
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-223 <BUL>
A:Cross-references: GB:U67591; GB:L77117; NID:g2862422; PIDN:AAB99514.1; PID:g15003899
C:Genetics:
A:Map position: REV1473617-1472946
C:Superfamily: conserved hypothetical protein MJ1501

Query Match 5.7%; Score 133; DB 2; Length 223;
Best Local Similarity 21.9%; Pred. NO. 0.0024;
Matches 46; Conservative 52; Mismatches 78; Indels 34; Gaps 7;

Qy 37 GSGDFAKSLIRLCIRCGYHVVGISRNPKFASEFPFHVVDV-----THHEDALT 84
Db 185 IDCGGLENAKVIEKITPLNLN 206

[illegible]

THIS PAGE BLANK (USPTO)